



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/080,980A

DATE: 09/12/2002
TIME: 10:15:41

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF4\09122002\J080980A.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company
5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,

6 K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE

8 <130> FILE REFERENCE: D0121 NP

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/080,980A

C--> 10 <141> CURRENT FILING DATE: 2002-02-21

10 <150> PRIOR APPLICATION NUMBER: US 60/270,132

11 <151> PRIOR FILING DATE: 2001-02-21

13 <150> PRIOR APPLICATION NUMBER: US 60/278,953

14 <151> PRIOR FILING DATE: 2001-03-27

16 <160> NUMBER OF SEQ ID NOS: 74

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 2052

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (121)..(1095)

29 <400> SEQUENCE: 1

30 cgtccggcgg ggcgcaggcg tgagcgagcg tccgggctcc ggggctccgg ggaaggcggt 60

32 tgcagctcct gagtgacgcg cggcttcctg ccactgtccc gcgcgcgcgc cctctctgtc 120

34 atg gct ctg gcg gac aca cgt gga tta ccc aac ggg ggc ggc ggc 168

35 Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly

36 1 5 10 15

38 ggg ggc agt ggc tcc tcg tcg tcc tcc gcg gag cca ccg ctc ttc 216

39 Gly Gly Gly Ser Gly Ser Ser Ser Ala Glu Pro Pro Leu Phe

40 20 25 30

42 ccc gac atc gtg gag ctg aac gtg ggg ggc cag gtg tac gtg acc cgg

43 Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg

44 35 40 45

46 cgc tgc acg gtg gtg tcg ccc gac tcg ctg ctc tgg cgc atg ttc 312

47 Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe

48 50 55 60

50 acg cag cag cag cag gag ctg gcc cgg gac agc aaa ggc cgc ttc 360

51 Thr Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe

52 65 70 75 80

54 ttt ctg gac cgg gac ggc ttc ctc ttc cgc tac atc ctg gat tac ctg

55 Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu

56 35 30 95

58 cgg gac ttg cag ctc gtg ctg ccc gac tac ttc ccc gag cgc agc cgg 456

59 Arg Asp Leu Gln Leu Val Pro Asp Tyr Phe Pro Glu Arg Ser Arg

60 100 105 110

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62	cgt cag cgc gag gcc gag tac ttc gag ctg cca gag	ctc gtg cgc cgc	504	
63	Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu	Leu Val Arg Arg		
64	115	120	125	
65	ctc ggg jcg ccc cag cag ccc ggc ccg ggg ccg	ccg ccc tcg egg cgc	552	
67	Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro	Pro Ser Arg Arg		
68	130	135	140	
70	ggg gtg cac aag gag ggc tcg ggt gac gag	ctg ctg ctt ggc	600	
71	Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu	Leu Leu Pro Leu Gly		
72	145	150	155	160
74	tac tcg gag ccc gaa cag cag gag ggc gac tct	gcc ggg gcg ccg tcg	648	
75	Tyr Ser Glu Pro Glu Gln Glu Gly Ala Ser Ala	Gly Ala Pro Ser		
76	165	170	175	
78	ccc acg ctg gag ctg gct acg cgc agt	ccg tcc ggg ggc gcg ggc	696	
79	Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser	Gly Gly Ala Ala Gly		
80	180	185	190	
82	ccg ctg ctc acg ccg tcc cag tcg ctg gac ggc	agg cgc tcg ggc	744	
83	Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly	Ser Arg Ser Gly		
84	195	200	205	
86	tac atc acc atc ggc tac cgc ggc tcc tac acc	atc ggg cgg gac gcg	792	
87	Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr	Ile Gly Arg Asp Ala		
88	210	215	220	
90	cag gcg gac gcc aag ttc cgg cga gtg gcg	ccg atc acc gtt tgc gga	840	
91	Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg	Ile Thr Val Cys Gly		
92	225	230	235	240
94	aag acg tcg ctg gcc aag gag gtg ttt ggg	gac acc ctg aac gaa agc	888	
95	Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp	Thr Leu Asn Glu Ser		
96	245	250	255	
98	ccg gac ccc gac cgt ccc ccg gag cgc tac acc	tcg cgc tat tac ctc	936	
99	Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr	Ser Arg Tyr Tyr Leu		
100	260	265	270	
102	aag ttc aac ttc ctg gag cag gcc ttc gac aag	ctg tcc gag tcg ggc	984	
103	Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys	Leu Ser Glu Ser Gly		
104	275	280	285	
106	ttc cac atg gtg gcg tgc agc tcc acg ggc	acc tgc gcc ttt gcc agc	1032	
107	Phe His Met Val Ala Cys Ser Ser Thr Gly	Thr Cys Ala Phe Ala Ser		
108	290	295	300	
110	agc acc gac cag agc gag aag atc tgg acc	agc tac acc gag tac	1080	
111	Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp	Thr Ser Tyr Thr Glu Tyr		
112	305	310	315	320
114	gtc ttc tgc agg gag tgagtcggcc agacccctc	gccactccag cgccccatgc	1135	
115	Val Phe Cys Arg Glu			
116	325			
118	ttctcctgcc cgagagatga ttacagagcc tcttgtccca	cctttgtccc ctggctgtcg	1195	
120	ccctccatt ctccccctcc agtagtagct gggtgagacc	tgtccggccca ccttccctcc	1255	
122	actacagaac ctgcagccgc aaatcctctg ggctgtttcg	tcttttttgg acctcctgaa	1315	
124	ccgagagaac ccagaggaac ccccaccca ccccccaccta	ccactccatg ctttctctac	1375	
126	tccctgcctc aaaccacccc tccccagat ggtacttcag	tttggatcta ttgggggagt	1435	
128	gtggccacag acgggggat gattgaattt ttcagaacct	gattggaccc tggtcaatgt	1495	
130	ggggaaagatt tcttgaaat cttctcaagc tcttatgact	cactgggggt ttaagagatc	1555	

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132	aggattgggtt	ccactgtctg	gggttagtgt	tttacaaggt	cattacacag	tcttttqac	1615										
134	ctctttgaa	ggtagagttt	tagaagggtg	gatggaagat	tctgagctg	gaattaggac	1675										
136	cccatggagg	cagtctcaa	accacccctc	ccccagatgg	tacttcagtt	tggatctatt	1735										
138	gggggagtgt	ggccacagac	cgggggatga	ttgaattgtt	cagaacrtga	ttggacccgtg	1795										
140	tccaatgtgc	ggaagatttc	cttgaatact	tctcaagctc	ttatgactca	ctgggggttt	1855										
142	aagagatcag	gattggttcc	actgtctggg	gttagtgttt	tacaaggctca	ttacacagtc	1915										
144	tttttgacct	cttttgaagg	tagagttta	gaaggctgga	ttgaagattc	tgagcctgga	1975										
146	attaggaccc	catggaggca	gttcagtaac	taaactaata	aagtttgaa	aagttacacg	2035										
148	aaaaaaaaaa	aaaaaaa					2052										
151	<210>	SEQ ID NO:	2														
152	<211>	LENGTH:	325														
153	<212>	TYPE:	PRT														
154	<213>	ORGANISM:	homo sapiens														
156	<400>	SEQUENCE:	2														
158	Met	Ala	Leu	Ala	Asp	Ser	Thr	Arg	Gly	Leu	Pro	Asn	Gly	Gly	Gly	Gly	
159	1				5					10							15
162	Gly	Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Ala	Glu	Pro	Pro	Leu	Phe		
163										20				25			30
166	Pro	Asp	Ile	Val	Glu	Leu	Asn	Val	Gly	Gly	Gln	Val	Tyr	Val	Thr	Arg	
167										35				40			45
170	Arg	Cys	Thr	Val	Val	Ser	Val	Pro	Asp	Ser	Leu	Leu	Trp	Arg	Met	Phe	
171										50				55			60
174	Thr	Gln	Gln	Pro	Gln	Glu	Leu	Ala	Arg	Asp	Ser	Lys	Gly	Arg	Phe		
175	65					70					75						80
178	Phe	Leu	Asp	Arg	Asp	Gly	Phe	Leu	Phe	Arg	Tyr	Ile	Leu	Asp	Tyr	Leu	
179										85				90			95
182	Arg	Asp	Leu	Gln	Leu	Val	Leu	Pro	Asp	Tyr	Phe	Pro	Glu	Arg	Ser	Arg	
183										100				105			110
186	Leu	Gln	Arg	Glu	Ala	Glu	Tyr	Phe	Glu	Leu	Pro	Glu	Leu	Val	Arg	Arg	
187										115				120			125
190	Leu	Gly	Ala	Pro	Gln	Gln	Pro	Gly	Pro	Gly	Pro	Pro	Pro	Ser	Arg	Arg	
191										130				135			140
194	Gly	Val	His	Lys	Glu	Gly	Ser	Leu	Gly	Asp	Glu	Leu	Leu	Pro	Leu	Gly	
195	145									150				155			160
198	Tyr	Ser	Glu	Pro	Glu	Gln	Glu	Gly	Ala	Ser	Ala	Gly	Ala	Pro	Ser		
199										165				170			175
202	Pro	Thr	Leu	Glu	Leu	Ala	Ser	Arg	Ser	Pro	Ser	Gly	Gly	Ala	Ala	Gly	
203										180				185			190
206	Pro	Leu	Leu	Thr	Pro	Ser	Gln	Ser	Leu	Asp	Gly	Ser	Arg	Arg	Ser	Gly	
207										195				200			205
210	Tyr	Ile	Thr	Ile	Gly	Tyr	Arg	Gly	Ser	Tyr	Thr	Ile	Gly	Arg	Asp	Ala	
211										210				215			220
214	Gln	Ala	Asp	Ala	Lys	Phe	Arg	Arg	Val	Ala	Arg	Ile	Thr	Val	Cys	Gly	
215	225									225				230			235
218	Lys	Thr	Ser	Leu	Ala	Lys	Glu	Val	Phe	Gly	Asp	Thr	Leu	Asn	Glu	Ser	
219										245				250			255
222	Arg	Asp	Pro	Asp	Arg	Pro	Pro	Glu	Arg	Tyr	Thr	Ser	Arg	Tyr	Tyr	Leu	
223										260				265			270
226	Lys	Phe	Asn	Phe	Leu	Glu	Gln	Ala	Phe	Asp	Lys	Leu	Ser	Glu	Ser	Gly	

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227 275 280 285
230 Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
231 290 295 300
234 Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
235 305 310 315 320
238 Val Phe Cys Arg Glu
239 325
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 228
244 <212> TYPE: PRT
245 <213> ORGANISM: Drosophila melanogaster
247 <400> SEQUENCE: 3
249 Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr
250 1 5 10 15
252 Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu
253 20 25 30
255 Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
256 35 40 45
258 Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
259 50 55 60
261 Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
262 65 70 75 80
264 Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
265 85 90 95
267 Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
268 100 105 110
270 Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
271 115 120 125
273 Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
274 130 135 140
276 Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
277 145 150 155 160
279 Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
280 165 170 175
282 Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
283 180 185 190
285 Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro
286 195 200 205
288 Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
289 210 215 220
291 Phe Ile Arg Asp
292 225
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 435
296 <212> TYPE: PRT
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 4
301 Gln Gln Gln Lys Lys Gly Thr Met Ala Leu Ser Gly Asn Cys Ser Arg
302 1 5 10 15

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304	Tyr	Tyr	Pro	Arg	Glu	Gln	Gly	Ser	Ala	Val	Pro	Asn	Ser	Phe	Pro	Glu
305			20				25									30
307	Val	Val	Glu	Leu	Asn	Val	Gly	Gly	Gln	Val	Tyr	Phe	Thr	Arg	His	Ser
308			35				40									45
310	Thr	Leu	Ile	Ser	Ile	Pro	His	Ser	Leu	Leu	Trp	Lys	Met	Phe	Ser	Pro
311			50				55									60
313	Lys	Arg	Asp	Thr	Ala	Asn	Asp	Leu	Ala	Lys	Asp	Ser	Lys	Gly	Arg	Phe
314	65				70					75						80
316	Phe	Ile	Asp	Arg	Asp	Gly	Phe	Leu	Phe	Arg	Tyr	Ile	Leu	Asp	Tyr	Leu
317				85					90							95
319	Arg	Asp	Arg	Gln	Val	Val	Leu	Pro	Asp	His	Phe	Pro	Glu	Lys	Gly	Arg
320			100				105									110
322	Leu	Lys	Arg	Glu	Ala	Glu	Tyr	Phe	Gln	Leu	Pro	Asp	Leu	Val	Lys	Leu
323			115				120									125
325	Leu	Thr	Pro	Asp	Glu	Ile	Lys	Gln	Ser	Pro	Asp	Glu	Phe	Cys	His	Ser
326	130				135					140						
328	Asp	Phe	Glu	Asp	Ala	Ser	Gln	Gly	Ser	Asp	Thr	Arg	Ile	Cys	Pro	Pro
329	145				150				155							160
331	Ser	Ser	Leu	Leu	Pro	Ala	Asp	Arg	Lys	Trp	Gly	Phe	Ile	Thr	Val	Gly
332				165				170								175
334	Tyr	Arg	Gly	Ser	Cys	Thr	Leu	Gly	Arg	Glu	Gly	Gln	Ala	Asp	Ala	Lys
335			180				185									190
337	Phe	Arg	Arg	Val	Pro	Arg	Ile	Leu	Val	Cys	Gly	Arg	Ile	Ser	Leu	Ala
338			195				200									205
340	Lys	Glu	Val	Phe	Gly	Glu	Thr	Leu	Asn	Glu	Ser	Arg	Asp	Pro	Asp	Arg
341			210				215									220
343	Ala	Pro	Glu	Arg	Tyr	Thr	Ser	Arg	Phe	Tyr	Leu	Lys	Phe	Lys	His	Leu
344	225				230				235							240
346	Glu	Arg	Ala	Phe	Asp	Met	Leu	Ser	Glu	Cys	Gly	Phe	His	Met	Val	Ala
347				245				250								255
349	Cys	Asn	Ser	Ser	Val	Thr	Ala	Ser	Phe	Ile	Asn	Gln	Tyr	Thr	Asp	Asp
350			260				265									270
352	Lys	Ile	Trp	Ser	Ser	Tyr	Thr	Glu	Tyr	Val	Phe	Tyr	Arg	Glu	Pro	Ser
353			275				280									285
355	Arg	Trp	Ser	Pro	Ser	His	Cys	Asp	Cys	Cys	Cys	Lys	Asn	Gly	Lys	Gly
356			290				295									300
358	Asp	Lys	Glu	Gly	Glu	Ser	Gly	Thr	Ser	Cys	Asn	Asp	Leu	Ser	Thr	Ser
359	305				310				315							320
361	Ser	Cys	Asp	Ser	Gln	Ser	Glu	Ala	Ser	Ser	Pro	Gln	Glu	Thr	Val	Ile
362				325				330								335
364	Cys	Gly	Pro	Val	Thr	Arg	Gln	Thr	Asn	Ile	Gln	Thr	Leu	Asp	Arg	Pro
365			340				345									350
367	Ile	Lys	Lys	Gly	Pro	Val	Gln	Leu	Ile	Gln	Gln	Ser	Glu	Met	Arg	Arg
368			355				360									365
370	Lys	Ser	Asp	Leu	Leu	Arg	Thr	Leu	Thr	Ser	Gly	Ser	Arg	Glu	Ser	Asn
371			370				375									380
373	Met	Ser	Ser	Lys	Lys	Lys	Ala	Val	Lys	Glu	Lys	Leu	Ser	Ile	Glu	Glu
374	385				390				395							400
376	Glu	Leu	Glu	Lys	Cys	Ile	Gln	Asp	Phe	Leu	Lys	Ile	Lys	Ile	Pro	Asp

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 15
Seq#:8; N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160
Seq#:8; N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495
Seq#:8; N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510
Seq#:8; N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525
Seq#:8; N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540
Seq#:8; N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678
Seq#:8; N Pos. 679,680,681,682,683,684,685,686,687,688

VARIABLE LOCATION SUMMARY
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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:6; Xaa Pos. 15

Seq#:8; N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160

Seq#:8; N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495

Seq#:8; N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510

Seq#:8; N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525

Seq#:8; N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540

Seq#:8; N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678

Seq#:8; N Pos. 679,680,681,682,683,684,685,686,687,688

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs. Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:432 M:341 W: (46) "n" cr "Xaa" used, for SEQ ID#:6 after pos.:0
L:547 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:547 M:341 W: (46) "n" cr "Xaa" used, for SEQ ID#:8 after pos.:120
L:559 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:559 M:341 W: (46) "n" cr "Xaa" used, for SEQ ID#:8 after pos.:480
L:561 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:561 M:341 W: (46) "n" cr "Xaa" used, for SEQ ID#:8 after pos.:540
L:565 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:565 M:341 W: (46) "n" cr "Xaa" used, for SEQ ID#:8 after pos.:660